

**results of BLAST****BLASTX 2.2.8 [Jan-05-2004]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1081974579-12914-23002148605.BLASTQ3

Query=

(623 letters)

translated

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

2,761,713 sequences; 776,183,611 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

No significant similarity found. For reasons why, [click here](#).

Lambda	K	H
0.318	0.135	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 170,867,881

Number of Sequences: 2761713

Number of extensions: 7756

Number of successful extensions: 7756

Number of sequences better than 10.0: 0

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 0

length of query: 623

length of database: 776,183,611

T: 12

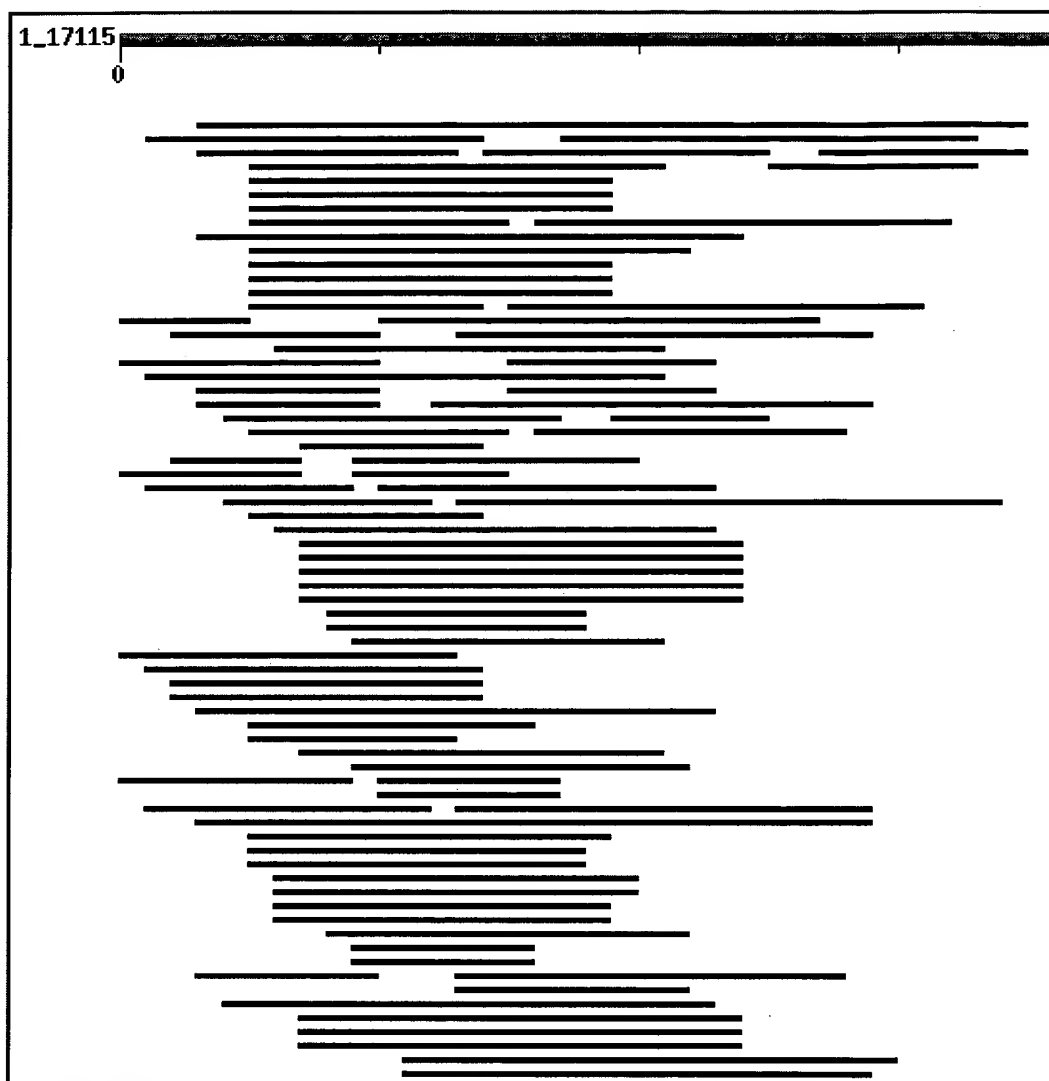
A: 40

X1: 16 (7.0 bits)

X2: 38 (15.0 bits)

X3: 64 (25.0 bits)

S1: 41 (22.0 bits)







Sequences producing significant alignments:

Score E
(bits) Value

gi 31240861 ref XP_320844.1 	ENSANGP00000017962 [Anopheles ...	31	2.6
gi 44368887 gb EAI78199.1 	unknown [environmental sequence]	30	4.7
gi 43888602 gb EAF98219.1 	unknown [environmental sequence]	28	20
gi 21242454 ref NP_642036.1 	MFS transporter [Xanthomonas a...	28	20
gi 44551201 gb EAK04439.1 	unknown [environmental sequence]	28	20
gi 42842225 gb EAA88537.1 	unknown [environmental sequence]	28	20
gi 43219805 gb EAC75458.1 	unknown [environmental sequence]	28	20
gi 44407058 gb EAJ05285.1 	unknown [environmental sequence]	28	20
gi 44043425 gb EAG81674.1 	unknown [environmental sequence]	28	27
gi 28900823 ref NP_800478.1 	3-hydroxy-3-methylglutaryl CoA...	28	27
gi 44372633 gb EAI80817.1 	unknown [environmental sequence]	28	27
gi 31203477 ref XP_310687.1 	ENSANGP00000023294 [Anopheles ...	28	27
gi 44386642 gb EAI90926.1 	unknown [environmental sequence]	28	27
gi 21231138 ref NP_637055.1 	MFS transporter [Xanthomonas c...	28	27
gi 44641669 gb EAK68491.1 	unknown [environmental sequence]	28	27
gi 23137395 ref ZP_00119101.1 	COG0475: Kef-type K+ transpo...	27	37
gi 21245069 ref NP_644651.1 	conserved hypothetical protein...	27	37
gi 24374681 ref NP_718724.1 	DnaJ domain protein [Shewanell...	27	49

Protein

gi 18398283 ref NP_565400.1	F-box family protein (FBL10) [...	27	49	
gi 10946860 ref NP_067441.1	TATA box binding protein (Tbp)...	27	49	L
gi 31983774 ref NP_858171.1	hypothetical protein [Shigella...	27	49	
gi 39584407 emb CAE72545.1	Hypothetical protein CBG19729 [...	27	49	
gi 34881098 ref XP_341168.1	similar to TAFI48 protein [Rat...	27	49	L
gi 42920963 gb EAB27554.1	unknown [environmental sequence]	27	49	
gi 28871387 ref NP_794006.1	hypothetical protein [Pseudomo...	27	49	
gi 46096284 gb EAK81517.1	hypothetical protein UM00132.1 [...	27	49	
gi 44010916 gb EAG63794.1	unknown [environmental sequence]	27	49	
gi 23128861 ref ZP_00110699.1	COG1020: Non-ribosomal pepti...	27	49	
gi 46198939 ref YP_004606.1	attH protein [Thermus thermoph...	27	49	
gi 31200971 ref XP_309433.1	ENSANGP00000008298 [Anopheles ...	27	66	
gi 9801567 gb AAF97943.2	cytochrome P450 CYP6N4v3 [Aedes a...	27	66	
gi 9801568 gb AAF97944.2	cytochrome P450 CYP6N4v4 [Aedes a...	27	66	
gi 33438763 ref NP_878045.1	Identified by homology to Ashb...	27	66	
gi 9801569 gb AAF97945.2	cytochrome P450 CYP6N4v5 [Aedes a...	27	66	
gi 28564982 gb AAO38684.1	truncated PDR5 [Saccharomyces kl...	27	66	
gi 15078968 ref NP_149719.1	256R [Invertebrate iridescent ...	27	66	
gi 15641102 ref NP_230734.1	periplasmic binding protein-re...	27	66	
gi 19114288 ref NP_593376.1	hypothetical protein [Schizosa...	27	66	
gi 41614963 ref NP_963461.1	NEQ168 [Nanoarchaeum equitans ...	27	66	
gi 43454600 gb EAD81974.1	unknown [environmental sequence]	27	66	
gi 40740521 gb EAA59711.1	hypothetical protein AN8089.2 [A...	27	66	
gi 9801570 gb AAF97946.2	cytochrome P450 CYP6N4v6 [Aedes a...	27	66	
gi 44328554 gb EAI49567.1	unknown [environmental sequence]	27	66	
gi 9801564 gb AAF97940.2	cytochrome P450 CYP6N4v1 [Aedes a...	27	66	
gi 43108888 gb EAC20512.1	unknown [environmental sequence]	26	88	
gi 729930 sp P16270 LECN_PEA	NONSEED LECTIN PRECURSOR >gi 3...	26	88	
gi 43489172 gb EAD99384.1	unknown [environmental sequence]	26	88	
gi 30260580 ref NP_842957.1	hypothetical protein [Bacillus...	26	88	
gi 43480485 gb EAD94982.1	unknown [environmental sequence]	26	88	
gi 22293495 emb CAD31853.1	putative chemosensory receptor ...	26	88	
gi 26987557 ref NP_742982.1	conserved hypothetical protein...	26	88	
gi 17230565 ref NP_487113.1	probable glycosyl transferase ...	26	88	
gi 13812138 ref NP_113265.1	chromosomal region maintenance...	26	88	
gi 43937826 gb EAG24250.1	unknown [environmental sequence]	26	88	
gi 100052 pir S20988	lectin - garden pea >gi 169172 gb AAA...	26	88	
gi 39587375 emb CAE75029.1	Hypothetical protein CBG22936 [...	26	88	
gi 21398366 ref NP_654351.1	hypothetical protein predicted...	26	88	
gi 5579428 gb AAD45549.1	SpcE [Streptomyces netropsis]	26	88	
gi 46108716 ref XP_381416.1	hypothetical protein FG01240.1...	26	119	
gi 42976288 gb EAB55098.1	unknown [environmental sequence]	26	119	
gi 630666 pir S40748	hypothetical protein F54C8.6 - Caenor...	26	119	
gi 32407800 ref XP_324399.1	hypothetical protein [Neurospo...	26	119	
gi 23612355 ref NP_703935.1	transportin [Plasmodium falcip...	26	119	
gi 15802965 ref NP_288995.1	Z3699 gene product [Escherichi...	26	119	
gi 7466358 pir A65018	hypothetical protein b2434 - Escheri...	26	119	
gi 17297993 dbj BAB78507.1	transportin [Plasmodium falcipa...	26	119	
gi 19113394 ref NP_596602.1	SNF2 family dna repair protein...	26	119	
gi 13476001 ref NP_107571.1	ABC transporter, substrate bin...	26	119	
gi 30020491 ref NP_832122.1	hypothetical protéin [Bacillus...	26	119	
gi 43818203 gb EAF63602.1	unknown [environmental sequence]	26	119	
gi 22298512 ref NP_681759.1	ORF_ID:tlr0969~probable membra...	26	119	
gi 31200297 ref XP_309096.1	ENSANGP000000019532 [Anopheles ...	26	119	
gi 23059042 ref ZP_00084044.1	COG0739: Membrane proteins r...	26	119	
gi 15964592 ref NP_384945.1	PROBABLE RIBONUCLEASE HII PROT...	26	119	
gi 28901509 ref NP_801164.1	putative ferrichrome ABC trans...	26	119	
gi 44010072 gb EAG63318.1	unknown [environmental sequence]	26	119	
gi 17553568 ref NP_499077.1	putative protein, with a trans...	26	119	L

gi 15240890 ref NP_195730.1 	expressed protein [Arabidopsis...	26	119	
gi 15889786 ref NP_355467.1 	AGR_C_4580p [Agrobacterium tum...	26	119	
gi 23307111 dbj BAC16541.1 	ferric vibrioferrin transport s...	26	119	
gi 43838017 gb EAF73243.1 	unknown [environmental sequence]	26	119	
gi 31208925 ref XP_313429.1 	ENSANGP00000019639 [Anopheles ...]	26	119	
gi 18860525 ref NP_573365.1 	CG7876-PA [Drosophila melanoga...	26	119	
gi 32565694 ref NP_497955.2 	serpentine Receptor, class G (...)	26	119	
gi 25342678 pir B88555	protein F54C8.6 [imported] - Caenor...	26	119	
gi 43713273 gb EAF11723.1 	unknown [environmental sequence]	25	159	
gi 15611696 ref NP_223347.1 	putative TYPE II DNA MODIFICAT...	25	159	
gi 15217347 gb AAK92685.1 	putative retrotransposon protein...	25	159	
gi 45185356 ref NP_983073.1 	ABR126Wp [Eremothecium gossypi...	25	159	
gi 32404370 ref XP_322798.1 	hypothetical protein (AL3900...	25	159	
gi 31196565 ref XP_307230.1 	ENSANGP00000024832 [Anopheles ...]	25	159	
gi 45184909 ref NP_982627.1 	AAR086Wp [Eremothecium gossypi...	25	159	
gi 17861760 gb AAL39357.1 	GH26215p [Drosophila melanogaster]	25	159	
gi 44081874 gb EAH02888.1 	unknown [environmental sequence]	25	159	
gi 31196563 ref XP_307229.1 	ENSANGP00000025224 [Anopheles ...]	25	159	
gi 15232200 ref NP_186830.1 	expressed protein [Arabidopsis...	25	159	
gi 43383694 gb EAD56739.1 	unknown [environmental sequence]	25	159	
gi 40742694 gb EAA61884.1 	hypothetical protein AN7698.2 [A...	25	159	
gi 13660729 gb AAK32960.1 	cytochrome P450 [Anopheles gambiae]	25	159	
gi 26336525 dbj BAC31945.1 	unnamed protein product [Mus mu...	25	159	

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|31240861|ref|XP_320844.1|](#) ENSANGP00000017962 [Anopheles gambiae]
[gi|21287767|gb|EAA00088.1|](#) ENSANGP00000017962 [Anopheles gambiae str. PEST]
 Length = 314

Score = 31.2 bits (66), Expect = 2.6

Identities = 19/47 (40%), Positives = 23/47 (48%), Gaps = 18/47 (38%)

Query: 4 WPFHFAFFH----Q-----ILATSTI--AMSHCRPTVYKQTSII 36
 WP+H A FH Q IL +TI A SHC VY Q+ +I
 Sbjct: 52 WPDHVALFHRKDAQEYACGGSILDENTILTA-SHC---VYTQSGVI 94

☐ >[gi|44368887|gb|EAI78199.1|](#) unknown [environmental sequence]
 Length = 563

Score = 30.3 bits (64), Expect = 4.7

Identities = 10/18 (55%), Positives = 12/18 (66%), Gaps = 4/18 (22%)

Query: 2 YKWPFHFHAF----FHQIL 15
 YK PF+F F FHQ+L
 Sbjct: 18 YKSPFNFI FGFLFFHQVL 35

☐ >[gi|43888602|gb|EAF98219.1|](#) unknown [environmental sequence]

Length = 190

Score = 28.2 bits (59), Expect = 20
Identities = 9/16 (56%), Positives = 10/16 (62%), Gaps = 5/16 (31%)

Query: 6 FHFAFF-----HQILA 16
FHFAFF QI+A
Sbjct: 128 FHFAFFFEFEGTQQIIA 143

☐ >[gi|21242454|ref|NP_642036.1|](#) MFS transporter [Xanthomonas axonopodis pv. citri]
[gi|21107899|gb|AAM36572.1|](#) MFS transporter [Xanthomonas axonopodis pv. citri str.
Length = 474

Score = 28.2 bits (59), Expect = 20
Identities = 10/17 (58%), Positives = 12/17 (70%)

Query: 6 FHFAFFHQILATSTIAM 22
F FAFF Q LA T+A+
Sbjct: 167 FAFAFFVQFLAVPTVAL 183

☐ >[gi|44551201|gb|EAK04439.1|](#) unknown [environmental sequence]
Length = 527

Score = 28.2 bits (59), Expect = 20
Identities = 10/19 (52%), Positives = 12/19 (63%), Gaps = 7/19 (36%)

Query: 6 FH----FAFFHQILATSTI 20
FH F+FFHQI S+I
Sbjct: 47 FHSFFKFSFFHQI---SSI 62

☐ >[gi|42842225|gb|EAA88537.1|](#) unknown [environmental sequence]
Length = 139

Score = 28.2 bits (59), Expect = 20
Identities = 7/11 (63%), Positives = 9/11 (81%)

Query: 4 WPFHFAFFHQI 14
WP+HF+F QI
Sbjct: 110 WPYHFSFIEQI 120

☐ >[gi|43219805|gb|EAC75458.1|](#) unknown [environmental sequence]
Length = 275

Score = 28.2 bits (59), Expect = 20
Identities = 10/19 (52%), Positives = 12/19 (63%), Gaps = 7/19 (36%)

Query: 6 FH----FAFFHQILATSTI 20
FH F+FFHQI S+I
Sbjct: 47 FHSFFKFSFFHQI---SSI 62

☐ >gi|44407058|gb|EAJ05285.1| unknown [environmental sequence]
Length = 531

Score = 28.2 bits (59), Expect = 20
Identities = 10/19 (52%), Positives = 12/19 (63%), Gaps = 7/19 (36%)

Query: 6 FH----FAFFHQILATSTI 20
FH FFFHQI S+I
Sbjct: 51 FHSFFKFSFFHQI---SSI 66

☐ >gi|44043425|gb|EAG81674.1| unknown [environmental sequence]
Length = 106

Score = 27.8 bits (58), Expect = 27
Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query: 6 FH----FAFFHQILATSTI 20
FH F FFHQI S+I
Sbjct: 1 FHSFFKFTFFHQI---SSI 16

☐ >gi|28900823|ref|NP_800478.1| 3-hydroxy-3-methylglutaryl CoA reductase [Vibrio p
RIMD 2210633]
gi|28809269|dbj|BAC62311.1| 3-hydroxy-3-methylglutaryl CoA reductase [Vibrio para
Length = 420

Score = 27.8 bits (58), Expect = 27
Identities = 10/18 (55%), Positives = 11/18 (61%), Gaps = 5/18 (27%)

Query: 11 FHQILATSTIAMSHCRPT 28
FH ILATS I +PT
Sbjct: 225 FHHILATSPI-----KPT 237

☐ >gi|44372633|gb|EAI80817.1| unknown [environmental sequence]
Length = 244

Score = 27.8 bits (58), Expect = 27
Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query: 6 FH----FAFFHQILATSTI 20
FH F FFHQI S+I
Sbjct: 130 FHSFFKFTFFHQI---SSI 145

☐ >gi|31203477|ref|XP_310687.1| ENSANGP00000023294 [Anopheles gambiae]
gi|30177923|gb|EAA45104.1| ENSANGP00000023294 [Anopheles gambiae str. PEST]
Length = 232

Score = 27.8 bits (58), Expect = 27
Identities = 15/36 (41%), Positives = 17/36 (47%), Gaps = 15/36 (41%)

Query: 4 WPFHFAFFHQ-----ILATSTI--AMSHC 25
WP+H A FHQ IL +TI A SHC
Sbjct: 1 WPHHAAIFHQKDKHKEYACGGSILDETTILTA-SHC 35

☐ >gi|44386642|gb|EAI90926.1| unknown [environmental sequence]
Length = 296

Score = 27.8 bits (58), Expect = 27
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 6 FHFAFFHQIL 15
F+FAFFH IL
Sbjct: 210 FYFAFFHSIL 219

☐ >gi|21231138|ref|NP_637055.1| MFS transporter [Xanthomonas campestris pv. campes
33913]
gi|21112775|gb|AAM40979.1| MFS transporter [Xanthomonas campestris pv. campestris
33913]
Length = 468

Score = 27.8 bits (58), Expect = 27
Identities = 10/18 (55%), Positives = 13/18 (72%)

Query: 6 FHFAFFHQILATSTIAMS 23
F FAFF Q LA ++A+S
Sbjct: 166 FAFAFFLQFLAVPSVALS 183

☐ >gi|44641669|gb|EAK68491.1| unknown [environmental sequence]
Length = 531

Score = 27.8 bits (58), Expect = 27
Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 7/19 (36%)

Query: 6 FH----FAFFHQILATSTI 20
FH F FFHQI S+I
Sbjct: 51 FHSFFKFTFFHQI---SSI 66

☐ >gi|23137395|ref|ZP_00119101.1| COG0475: Kef-type K+ transport systems, membrane
[Cytophaga hutchinsonii]
Length = 414

Score = 27.4 bits (57), Expect = 37
Identities = 13/35 (37%), Positives = 16/35 (45%), Gaps = 19/35 (54%)

Query: 7 HF---AFF-----HQIL-----ATSTIAM 22
HF AFF H++L +TSTIAM
Sbjct: 264 HFVIGAFFGAMLLSHELLGKENFHIVEKSTSTIAM 298

☐ >[gi|21245069|ref|NP_644651.1|](#) conserved hypothetical protein [Xanthomonas axonop
str. 306]
[gi|21110802|gb|AAM39187.1|](#) conserved hypothetical protein [Xanthomonas axonopodis
str. 306]
Length = 129

Score = 27.4 bits (57), Expect = 37
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 3 KWPFFHFAFF 11
KW F FAFF
Sbjct: 12 KWQFRFAFF 20

☐ >[gi|24374681|ref|NP_718724.1|](#) DnaJ domain protein [Shewanella oneidensis MR-1]
[gi|24349326|gb|AAN56168.1|](#) DnaJ domain protein [Shewanella oneidensis MR-1]
Length = 402

Score = 26.9 bits (56), Expect = 49
Identities = 9/11 (81%), Positives = 9/11 (81%), Gaps = 1/11 (9%)

Query: 6 FHFAFFHQILA 16
FH AFF QILA
Sbjct: 170 FH-AFFEQILA 179

☐ >[gi|18398283|ref|NP_565400.1|](#) F-box family protein (FBL10) [Arabidopsis thaliana
[gi|25372906|pir||B84547](#) hypothetical protein At2g17020 [imported] - Arabidopsis t
[gi|6598359|gb|AAF18597.1|](#) unknown protein [Arabidopsis thaliana]
[gi|13605809|gb|AAK32890.1|](#) At2g17020 [Arabidopsis thaliana]
[gi|22137200|gb|AAM91445.1|](#) At2g17020/At2g17020 [Arabidopsis thaliana]
Length = 656

Score = 26.9 bits (56), Expect = 49
Identities = 9/14 (64%), Positives = 12/14 (85%), Gaps = 1/14 (7%)

Query: 11 FHQILATSTIAMSH 24
FH ILAT T+++SH
Sbjct: 370 FHDILAT-TLSLSH 382

☐ >[gi|10946860|ref|NP_067441.1|](#) ☒ TATA box binding protein (Tbp)-associated factor
A [Mus musculus]
[gi|1842204|emb|CAA71091.1|](#) ☒ TAFI48 protein [Mus musculus]
[gi|38174627|gb|AAH61106.1|](#) ☒ TATA box binding protein (Tbp)-associated factor, RN
A [Mus musculus]
Length = 453

Score = 26.9 bits (56), Expect = 49
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 4 WP-FHFAFF 11
WP FHF+FF
Sbjct: 380 WPAFHFSFF 388

☐ >[gi|31983774|ref|NP_858171.1|](#) hypothetical protein [Shigella flexneri 2a]
[gi|18462766|gb|AAL72538.1|](#) hypothetical protein [Shigella flexneri 2a]
Length = 139

Score = 26.9 bits (56), Expect = 49
Identities = 11/17 (64%), Positives = 13/17 (76%), Gaps = 2/17 (11%)

Query: 14 ILATSTIAMSHCRPTVY 30
ILA+S I+M H R TVY
Sbjct: 87 ILASSKISMLH-R-TVY 101

☐ >[gi|39584407|emb|CAE72545.1|](#) Hypothetical protein CBG19729 [Caenorhabditis briggsae]
Length = 169

Score = 26.9 bits (56), Expect = 49
Identities = 10/17 (58%), Positives = 12/17 (70%), Gaps = 5/17 (29%)

Query: 5 PFHFAPF---FHQILATS 18
PFHFA+ FH +ATS
Sbjct: 50 PFHFAYEAPFH--IATS 64

☐ >[gi|34881098|ref|XP_341168.1|](#) ☒ similar to TAFI48 protein [Rattus norvegicus]
Length = 238

Score = 26.9 bits (56), Expect = 49
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

Query: 4 WP-FHFAPF 11
WP FHF+FF
Sbjct: 165 WPAFHFSFF 173

☐ >[gi|42920963|gb|EAB27554.1|](#) unknown [environmental sequence]
Length = 245

Score = 26.9 bits (56), Expect = 49
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 10 FFHQILA 16
FFHQILA
Sbjct: 108 FFHQILA 114

☐ >[gi|28871387|ref|NP_794006.1|](#) hypothetical protein [Pseudomonas syringae pv. tom] [gi|28854638|gb|AAO57701.1|](#) hypothetical protein PSPT04245 [Pseudomonas syringae p str. DC3000]
Length = 1111

Score = 26.9 bits (56), Expect = 49
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 8 FAFHHQIL 15
FAFHHQ+L
Sbjct: 728 FAFHHQLL 735

☐ >gi|46096284|gb|EAK81517.1| hypothetical protein UM00132.1 [Ustilago maydis 521]
Length = 506

Score = 26.9 bits (56), Expect = 49
Identities = 10/17 (58%), Positives = 14/17 (82%), Gaps = 1/17 (5%)

Query: 18 STIAMSHCRPTVYKQTS 34
S+I+ SHCRP Y++TS
Sbjct: 21 SSISSSHCRPD-YRRTS 36

☐ >gi|44010916|gb|EAG63794.1| unknown [environmental sequence]
Length = 170

Score = 26.9 bits (56), Expect = 49
Identities = 10/21 (47%), Positives = 11/21 (52%), Gaps = 8/21 (38%)

Query: 2 YKWPFHFAFHHQILATSTIAM 22
Y WPF+F ILA I M
Sbjct: 124 YMWPFYF-----ILA---IGM 136

☐ >gi|23128861|ref|ZP_00110699.1| COG1020: Non-ribosomal peptide synthetase module
proteins [Nostoc punctiforme]
Length = 2181

Score = 26.9 bits (56), Expect = 49
Identities = 8/12 (66%), Positives = 8/12 (66%)

Query: 10 FFHQILATSTIA 21
FFH I A TIA
Sbjct: 595 FFHHIFANPTIA 606

☐ >gi|46198939|ref|YP_004606.1| attH protein [Thermus thermophilus HB27]
gi|46196563|gb|AAS80979.1| attH protein [Thermus thermophilus HB27]
Length = 335

Score = 26.9 bits (56), Expect = 49
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 2/11 (18%)

Query: 1 PYKWPFHFAFF 11
PY FHFAFF
Sbjct: 59 PY--AFHFAFF 67

☐ >gi|31200971|ref|XP_309433.1| ENSANGP00000008298 [Anopheles gambiae]